

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 40 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOS: 2, 4, 6, 30, 32, and 34,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

2. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 150 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOS: 8, 10, 36, and 38,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

3. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 200 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOS: 12 and 40,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

4. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 175 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOS: 14, 16, 18, 42, 44, and 46,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

5. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NOS: 20, 22, 24, 26, 28, 48, 50, 52, 54, and 56,

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

6. The isolated polynucleotide of Claim 1, Claim 2, Claim 3, Claim 4, or Claim 5, wherein the first nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, and 55 that codes for the polypeptide selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, and 56.

7. The isolated polynucleotide of Claim 1, Claim 2, Claim 3, Claim 4, or Claim 5 wherein the nucleotide sequences are DNA.

8. The isolated polynucleotide of Claim 1, Claim 2, Claim 3, Claim 4, or Claim 5 wherein the nucleotide sequences are RNA.

9. A chimeric gene comprising the isolated polynucleotide of Claim 1, Claim 2, Claim 3, Claim 4, or Claim 5 operably linked to suitable regulatory sequences.

10. An isolated host cell comprising the chimeric gene of Claim 9.

11. A host cell comprising an isolated polynucleotide of Claim 1, Claim 2, Claim 3, Claim 4, or Claim 5.

12. The host cell of Claim 11 wherein the host cell is selected from the group consisting of yeast, bacteria, plant, and virus.

13. A virus comprising the isolated polynucleotide of Claim 1, Claim 2, Claim 3, Claim 4, or Claim 5.

14. A polypeptide of at least 40 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 30, 32, and 34.

15. A polypeptide of at least 150 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:8, 10, 36, and 38.

16. A polypeptide of at least 200 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:12 and 40.

17. A polypeptide of at least 175 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:14, 16, 18, 42, 44, and 46.

18. A polypeptide selected from the group consisting of SEQ ID NOs:20, 22, 24, 26, 28, 48, 50, 52, 54, and 56.

19. A method of selecting an isolated polynucleotide that affects the level of expression of a proteinase polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from an isolated polynucleotide of Claim 1, Claim 2, Claim 3, Claim 4, or Claim 5;

(b) introducing the isolated polynucleotide into a plant cell;

(c) measuring the level of a polypeptide in the plant cell containing the polynucleotide; and

(d) comparing the level of polypeptide in the plant cell containing the isolated polynucleotide with the level of polypeptide in a plant cell that does not contain the isolated polynucleotide.

20. The method of Claim 19 wherein the isolated polynucleotide consists of a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9,11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, and 55 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, and 56.

21. A method of selecting an isolated polynucleotide that affects the level of expression of a proteinase polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide of Claim 1, Claim 2, Claim 3, Claim 4, or Claim 5;

(b) introducing the isolated polynucleotide into a plant cell;

(c) measuring the level of polypeptide in the plant cell containing the polynucleotide; and

(d) comparing the level of polypeptide in the plant cell containing the isolated polynucleotide with the level of polypeptide in a plant cell that does not contain the polynucleotide.

22. A method of obtaining a nucleic acid fragment encoding a proteinase polypeptide comprising the steps of:

(a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9,11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, and 55 and the complement of such nucleotide sequences; and

(b) amplifying a nucleic acid sequence using the oligonucleotide primer.

23. A method of obtaining a nucleic acid fragment encoding a proteinase polypeptide comprising the steps of:

(a) probing a cDNA or genomic library with an isolated polynucleotide comprising at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9,11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, and 55 and the complement of such nucleotide sequences;

(b) identifying a DNA clone that hybridizes with the isolated polynucleotide;

(c) isolating the identified DNA clone; and

(d) sequencing the cDNA or genomic fragment that comprises the isolated DNA clone.

24. A composition comprising the isolated polynucleotide of Claim 1, Claim 2, Claim 3, Claim 4, or Claim 5.

25. A composition comprising the isolated polynucleotide of Claim 14, Claim 15, Claim 16, Claim 17, or Claim 18.

26. An isolated polynucleotide comprising the nucleotide sequence having at least one of 30 contiguous nucleotides derived from a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9,11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, and 55 and the complement of such sequences.

27. An expression cassette comprising an isolated polynucleotide of Claim 1, Claim 2, Claim 3, Claim 4, or Claim 5 operably linked to a promoter.

28. A method for positive selection of a transformed cell comprising:

(a) transforming a host cell with the chimeric gene of Claim 9 or an expression cassette of Claim 27; and

(b) growing the transformed host cell under conditions which allow expression of the polynucleotide.

29. The method of Claim 28 wherein the plant cell is a monocot.

30. The method of Claim 28 wherein the plant cell is a dicot.